

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE; 701 AA; 7826 MW; 94AC6CEB42CC992F CRC64;

Query Match 98.8%; Score 2161; DB 4; Length 701;
 Best Local Similarity 97.3%; Pred. No. 1. 5e-202;
 Matches 395; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 ANAFLXXLRPGSLRXCKXXQCSFXAXIKDXARTKLEWISYSDGDOCASSPCQNGS 60
 DB 61 ANAFLBELRPGSLERECKEBOCSFEARELFKDAERTKLFWISYSDGDOCASSPCQNGS 120

QY 61 CKDQLOSYICFCPLPREFGRGCETHKDQDLCIVNGGCEQYCSDHGTGRSCRGHESL 120
 121 CKDQLOSYICFCPLPREFGRGCETHKDQDLCIVNGGCEQYCSHTGKRSRGCHESL 180

QY 121 LADGVSTCPVVEYPOGKIPITLEKRNASKRQGRIVGGKVKCPGKCPWQVLLVNGAQLGG 180
 181 LADGVSTCPVVEYPOGKIPITLEKRNASKRQGRIVGGKVKCPGKCPWQVLLVNGAQLGG 180

QY 181 TLINTIWVVAACHCFDKIKRNWLNLAVLGEHDLSERHDDEQSRRQAQVITPSTYVPGTN 240
 241 TLINTIWVVAACHCFDKIKRNWLNLAVLGEHDLSERHDDEQSRRQAQVITPSTYVPGTN 300

QY 241 HDIALLRHQPVLTDHVPLCPERTSERVLAFLVSGQQLDRGATALEMLV 300
 301 HDIALLRHQPVLTDHVPLCPERTSERVLAFLVSGQQLDRGATALEMLV 360

QY 301 NVPRLMTQDQLOQRKVGDSNPTEMFCAGYSDGSKSCAGGGPHATHYRGTWLTG 360
 361 NVPRLMTQDQLOQRKVGDSNPTEMFCAGYSDGSKSCAGGGPHATHYRGTWLTG 420

QY 361 IVSWGQGATVGHGVYVTRVSQIENIQLKMSSEPRPVLLRAPP 406
 421 IVSWGQGATVGHGVYVTRVSQIENIQLKMSSEPRPVLLRAPP 466

RESULT 2

ID 061109 PRELIMINARY; PRT; 446 AA.
 AC 061109;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Coagulation factor VII.
 GN FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96276538; PubMed=8701412;
 RA Iduocie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487(1996).
 CC -I SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRIPSIN FAMILY.
 DR EMBL; U44795; AAC52570.1; -.
 DR HSSP; P08109; 1FAK.
 DR MEROPS; S01.215; -.
 DR MGI; MGI:09325; F7.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR00134; Chymotrypsin.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR00561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GIA_blood.
 DR InterPro; IPR01254; Ser_Protease_Try.

DR InterPro; IPR000294; VITK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gta; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PR0072; CHYMOTRYPSIN.
 DR PR0001; GLABLOOD.
 DR SMART; SM00119; EGF_Ca; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00069; Gta; 1.
 DR SMART; SM0020; TRY_P-SPC; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS0001; ASX_HIDROYL; UNKNOWN_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS0187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBONYLATION; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Calcium binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat; Serine Protease; 446 AA; 50318 MW; 482FD09BEBFDA6870 CRC64;

Query Match 71.3%; Score 1558.5; DB 11; Length 446;
 Best Local Similarity 67.8%; Pred. No. 7. 1e-144;
 Matches 274; Conservative 46; Mismatches 83; Indels 1; Gaps 1;

QY 1 ANAFLXXLRPGSLRXCKXXQCSFXAXIKDXARTKLEWISYSDGDOCASSPCQNGS 60
 DB 42 ANSLEELWPGSLERECKEBOCSFEARELFKDAERTKLFWISYSDGDOCASSPCQNGT 101

QY 61 CKDQLOSYICFCPLPREFGRGCETHKDQDLCIVNGGCEQYCSDHGTGRSCRGHESL 120
 102 CODHLKSYICFCPLPREFGRGCETHKDQDLCIVNGGCEQYCSHTGKRSRGCHESL 161

QY 121 LADGVSTCPVVEYPOGKIPITLEKRNASKRQGRIVGGKVKCPGKCPWQVLLVNGAQLGG 180
 162 QPDEVSKPKVEYPCGRIPVVEKRNSSRSGRIVGGVCKPGECPROAVKINGLLCGA 221

QY 181 TLINTIWVVAACHCFDKIKRNWLNLAVLGEHDLSERHDDEQSRRQAQVITPSTYVPGTN 240
 222 VLDARNITVTAHCFDINRIVNGNITVGMERDESEKGDDEQNRVTVQIMPKYIRKIN 281

QY 241 HDIALLRHQPVLTDHVPLCPERTSERVLAFLVSGQQLDRGATALEMLV 300
 282 HDIALLRHQPVFTDHWPLCPKSFSENTLARIFRSVYSGQQLDRGATALEMSI 341

QY 301 NVPRLMTQDQLOQRKVGDSNPTEMFCAGYSDGSKSCAGGGPHATHYRGTWLTG 360
 342 EVPRLMTOCDLHAKHSNTPTKITEFMFCAGYSDGSKSCAGGGPHATHYRGTWLTG 401

QY 361 IVSWGQGATVGHGVYVTRVSQIENIQLKMSSEPRPVLLRAP 404
 402 IVSWGEGCAAGHIGHVYTRVSQIENIQLKMSSEPRPVLLRAP 444

RESULT 3

Q90YK1 PRELIMINARY; PRT; 433 AA.
 ID Q90YK1
 AC 090YK1
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Coagulation factor VII.
 OS Brachydonto rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OC NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21353085; PubMed=11459993;
 RA Sheehan J., Tempier M., Gregory M., Hanumanthaiah R., Troyer D.,

RA	Phan T., Thankavel B., Jagadeeswaran P.,	RT	"Identification and structural analysis of four serine proteases in a
RT	"Demonstration of the extrinsic coagulation pathway in teleostei:	RT	monotreme, the platypus, Ornithorhynchus anatinus.;"
RT	Identification of zebrafish coagulation factor VII.";	RL	Immunogenetics 52:19-28 (2000).
RL	Proc. Natl. Acad. Sci. U.S.A. 98:8768-8773 (2001).	CC	-1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
DR	EMBL: AV04045; AK74192.1; -.	CC	TRIPSIN FAMILY.
DR	InterPro: IPR000561; EGF-like.	DR	EMBL: AF215654; AAC00453.1; -.
DR	InterPro: IPR000742; EGF 2.	DR	HSSP: P00742; 1XB.
DR	InterPro: IPR001881; EGF_Ca.	DR	MEROPS: S01.216; -.
DR	InterPro: IPR001284; Ser_protease_Try.	DR	InterPro: IPR000152; Asx-hydroxyl.
DR	InterPro: IPR002024; VitK_dep_GLA.	DR	InterPro: IPR001314; Chymotripsin.
DR	Pfam: PF00008; EGF; 2.	DR	InterPro: IPR000561; EGF-like.
DR	Pfam: PF00594; gta; 1.	DR	InterPro: IPR000742; EGF 2.
DR	Pfam: PF00089; trypsin; 1.	DR	InterPro: IPR01881; EGF_Ca.
DR	PROSITE: PS00022; EGF_Ca; 2.	DR	InterPro: IPR02383; GLA_blood.
DR	PROSITE: PS01186; EGF; 2; UNKNOWN_1.	DR	InterPro: IPR001254; Ser_protease_Try.
DR	PROSITE: PS00011; GLU_CARBOXYLATION; UNKNOWN_1.	DR	InterPro: IPR00094; VitK_dep_GLA.
DR	PROSITE: PS00240; TRYPSIN_DOM; 1.	DR	Pfam: PF00008; EGF; 2.
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.	DR	Pfam: PF00594; gta; 1.
DR	PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.	DR	PRINTS: PRO0722; CHYMOTRIPSPIN.
KW	Hydrolase; Serine protease.	DR	PRINTS: PRO0001; GLABLOOD.
SEQUENCE	433 AA; 48680 MN; CD9D1B179601BAAC CRC64;	DR	SMART: SM00001; EGF-like; 2.
Query Match	Best Local Similarity 45.9%; Score 913.5; DB 13; Length 433; Matches 178; Conservative 59; Mismatches 138; Indels 13; Gaps 6;	DR	SMART: SM00059; GLA; 1.
Oy	8 LRGGLRXXCKXXQCSFXKARXIFKDAKXTRKLFWISYSPGQDQASSPQNGGSKDQ-LQ 66	DR	SMART; SM0020; TRYPSIN_SPEC; 1.
Db	46 LKIGNLEREBCLEEKSYBEEAREVFEHTAEINPFWKDYVKDHCAASPPCHDGLCTTQNAQD 105	DR	PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
Oy	67 SYFCFCFLPAREFGRNCETHKDDQL-ICVNENGCGEQYCSDHTGKRSRCHEGSSLADGV 125	DR	PROSITE: PS01186; EGF; 2; UNKNOWN_1.
Db	106 SYMCICAPGFGSRHCEQSITGVDLSDCLINDGCEHFCBTDG-RRNCSCADGYTLDSRQ 164	DR	PROSITE: PS00117; EGF_Ca; 1.
Oy	126 SCPTVEPCKPILERRNASKPQ---GRIGGVKVERPKGECEPWQVQVILLVNGAQLCGT 181	DR	PROSITE: PS00240; TRYPSIN_DOM; 1.
Db	165 KCRSHVEPCKGVPLQDQGAADHQVDSLRSVGGSECPKGHPQWQVLLKYGKFGFCGGV 224	DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
Oy	182 LINTIWIIVSAHCFDKIKNMRNLIAVLGEDHLDSEHGDQBSRRQAVIIPSTVPGTNH 241	DR	PROSITE: PS00135; TRYPSIN_SER; 1.
Db	225 IYKPTWILTAHGLEKLK-VKELRIVAGEHDLVEDGEDEBQLQDMDTHPAYSETADS 283	DR	HYdrolase; Serine protease.
Oy	242 DIALLRHOPVVLTDHVPLCPERTSERTLAFVRSVLSVQGLDQGATAELMVN 301	DR	SEQUENCE 469 AA; 52196 MN; 4C66C230D0758F6A CRC64;
Db	284 DIALLRKTPIVSIVYAVPVCPLPREMARELAVSKHVNWSNGKRSRBDGPTSLRLL 343	Query Match	Best Local Similarity 39.5%; Score 863; DB 6; Length 469; Matches 168; Conservative 72; Mismatches 143; Indels 54; Gaps 7;
Oy	302 VRLMTQDQLQSKRKGDSNTEYMFAGYSDGSKDCKGDSGGPHATHYRGWYLIGI 361	Db	1 ANAFLXXLPRGLSLRXXQCSFXKARXIFKDAKXTRKLFWISYSPGQDQASSPQNGG 60
Db	344 VPIRTOBCVQTS-----NLTJUSNMFCAGYIEGRQDCKGDSGGPLVTRYRDTAFLIGI 398	Db	41 ANSEFEELKKGNLEREBCNECNETCSYBEEAREVFEHTAEINPFWKDYVKDHCAASPPCHDQ 100
Oy	362 VSWGOGGATVGHGVYVRSVQYIEWLQR 389	Db	61 CKDQDOSYCFCLPAREFGRNCETHKDDQLICVNGCGEQYCSDHTGKRSRCHEGSSL 120
Db	399 VSWKGKGCARRPGSYGIYRVSNLQWQR 426	Db	101 CKDGLAEYTCLCGAGYEGKNDT--TTWICSLNQGDCBDFCKSVNVT-VCSAOGVIL 157
RESULT 4		Db	121 LADGVSCTPVEPCKKPI-LEKRNASKPQG----- 151
O9GMD9	PRELIMINARY: PRT: 469 AA.	Db	158 GDDQKSCITBTPPEPCKLVLGRRRSRELPEEVDGDNAAHVAEDVLEATENPPEAEPPDN 217
ID	O9GMD9	Db	152 -----RIVGGKVCPKGRCPPQVLL--VNGAOLCGSTLINTIWVSAHCFDK 197
AC	O9GMD9; 01-MAR-2001 (TREMBrel. 16, Created)	Db	218 TTAEGPGENALVRRVGGRECHDGECPWQWALLVNDENGQFCGGTILNEYVYIISAAHCWQH 277
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)	Qy	198 IKNWRLIATLVLGEBDLSHGDQBSRRQAVIIPSTVPGTNHDIALLRQPVWLTDH 257
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)	Db	278 AKRKF---VRGERDTEKKDSSEMAHEVEKVTVHSKEVKVTDFFDIAVIKLKPITPRMN 334
DE	Coagulation factor X.	Qy	258 VVPLCPERTSERTLAFVRSVLSVQGLDQGATAELMVN 317
OS	Ornithorhynchus anatinus (Duckbill Platypus).	Db	335 VSPLCPERKWDIAIMNOKAGVYSGFGRVHENGPSVTKLMEVPPVETTCQSS-- 391
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus. NCBI TaxID: 9258; [1]	Qy	318 GDSPNITEYMFAGYSDGSKDCKGDSGGPHATHYRGWYLIGI 377
OX	SEQUENCE FROM N.A.	Db	392 --SFDITENMFAGYSDPREDACQGDGDSGGPHATHYRGWYLIGI 449
RN	REMLINE-21015017; PubMed-11132153;	Qy	378 TRYSOYIWLQKMLRE 394
RX	Poofarshar M., Aveskogh M., Munday B., Hellman L.;	Db	450 TKAFLSWIKRMQRQ 466

CC TRYPsin FAMILY
 DR EMBL: X9807; CAA56202; 1; -
 DR HSP; P00742; 1XKA.
 DR MEROPS; S01.216; -
 DR InterPro; IPR00152; ASX_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR00294; VITK_dep,GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF0089; trypsin; 1.
 DR PRINTS; PR00022; CHYMOtrypsin.
 DR SMART; SM0019; EGF_Ca; 1.
 DR SMART; SM0001; EGF_like; 1.
 DR SMART; SM0059; GLA; 1.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01186; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYFIN_DOM; 1.
 DR PROSITE; PS00134; TRYPRIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPRIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease.
 SQ 482 AA; 54265 MW; 0284678E395A698 CRC64;

Query Match 38.0%; Score 831.5; DB 11; Length 482;
 Matches 159; Conservative 83; Mismatches 144; Indels 55; Gaps 7; FT
 QY 1 ANAFLXXLRPGSLARXXKXXCSFXXARXKFDAXRTKLFWISYSDGDCASSPCQNGGS 60
 41 ANSFFEEFKKGNLRECVCBEICSPFEEAREFEDNEKTFEFWNKYEKGDOCESSPCONGE 100
 QY 61 CKDQDQSYCFCFLAFEGENCEETHKDQDLCIVNGGCEQYCSHTGKVRKSCCHEGYSL 120
 101 CRDLSGGSYCTCTGCFEGKNCFLFV-RKLCSLONGDDOCFCREBONSY-VCSCAKGYZFL 157
 121 LADSVSCTPVEVFCGKTI-----
 158 GNDKSKSCLUSTAPFCGKTKNGRAKRSVALNTSNSERPDLMPPDILYPTESSELNL 217
 QY 145 NASPQG-----RTVGGKVCPKPCPQYVLLVNGAQ---LCCG3LTINTIIVVSAARCFD 196
 218 NKTEPEANSDDVIRIVGGOECKRGCPCPWALLFSSDEETGFCGGTILNEFYILAAHCLH 277
 QY 197 KIKKWRNLIAVLGHDLSHDGQSRRAVQVITPSTVPGTINHMDIALRLHQPVWTD 256
 278 QAKFK--VRVGDLNTEDGGAVMHEVDMDITKHNKFQDRTYFDIAMRLKPTIRE 334
 QY 257 HVVFLCLPRTFSERTLAFLVFRFSIYSGWQLDRGATALEMVNVPRIMTDCQGSRK 316
 Db 335 NVAFACPLQDKWALATMWTQTKGIVSGGGRRTHEGRGOSKVKMNEVYPVDRWTC---R 389
 QY 317 VGDSPNITEVMFCAGYSGDSKDSKGDSGGPHATHYRGWYLTCGIVSNGQCATVGHFGV 376
 QY 390 LSTSFSTONMFQCGYDQKEDACQGDGGSGPFGHTRFKOTIFVIGIVSNEGGCKRGKGYI 449
 QY 377 YTRVSOYIENLQKLMRSEPRP 397
 Db 450 YTKVTAFLKWDIDRSMKARVGP 470

AC 088947;
 DT 01-NOV-1998 (TREMBlre. 08, Created)
 DT 01-NOV-1998 (TREMBlre. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlre. 20, Last annotation update)
 DE Coagulation factor X precursor.
 GN F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=57BL6_X_CBA; TISSUE=LIVER;
 RX MEDLINE=9834933; Pubmed=9684791;
 RA Liang Z.; Cooper A.; Bedford M.E.; Carmeliet P.; Collen D.;
 RA Castellino F.J.; Rosen E.D.;
 RT "Cloning and characterization of a cDNA encoding murine coagulation factor X";
 RT Thromb. Haemost. 80:87-91(1998).
 RL RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SJ;
 RA Cooper A.; Liang Z.; Castellino F.J.; Rosen E.D.;
 RT "Cloning and Characterization of the Murine Factor X Gene.";
 RL Thromb. Haemost. 0:0-0(2000).
 CC -; SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL: AF087644; AAC36345; 1; -
 DR EMBL: AF211347; AF22980; 1; -
 DR HSSP; P00742; 1XKA.
 DR MEROPS; S01.216; -
 DR MGD; MGI; 103107; F10.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR00134; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR00042; EGF_2.
 DR InterPro; IPR001831; EGF_Ca.
 DR InterPro; IPR00283; GLA_blood.
 DR InterPro; IPR001284; Ser_protease_Try.
 DR Pfam; PR00008; EGF; 2.
 DR Pfam; PR00594; gla; 1.
 DR PROSITE; PS00722; CHYMOtrypsin.
 DR PRINTS; PR00001; GLA_blood.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00001; EGF_like; 1.
 DR SMART; SM00059; GLA; 1.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00134; TRYPRIN_HIS; 1.
 DR PROSITE; PS00135; TRYPRIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat; Serine protease; Signal.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 481 COAGULATION FACTOR X.
 SQ SEQUENCE 481 AA; 54018 MW; 8AC09B5E5FD271E CRC64;

Query Match 38.0%; Score 830; DB 11; Length 481;
 Best local Similarity 36.6%; Pred. No 1.5e-72;
 Matches 161; Conservative 83; Mismatches 142; Indels 54; Gaps 8; FT
 QY 1 ANAFLXXLRPGSLARXXKXXCSFXXARXKFDAXRTKLFWISYSDGDCASSPCQNGGS 60
 41 ANSFFEEFKKGNLRECVCBEICSPFEEAREFEDNEKTFEFWNKYEKGDOCESSPCONGA 100
 QY 61 CKDQDQSYCFCFLAFEGENCEETHKDQDLCIVNGGCEQYCSHTGKVRKSCCHEGYSL 120

101 CRDGIGGYTCSEGGKNCLELV - RKLCLRDGDCDFCREEQNSV - VSCCAGYFL 157

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00022; EGF_LIKE; 1.

KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat; Serine protease.

QY SEQUENCE 481 AA; 54004 MW; BD88E968A0B8E7F CRC64;

218 NETOPERSSDLVRLVYGRCKDGCPWQVLL - VNGAQLCGGLINTIIVWSAHCDF 197

198 IKNWRNLIAVIGEHDLESEHDEQDSRVAQVITPSTVPGTNHDAILRLHQPVVLHD 257

278 ARRF -- VRVGDRTKEKEGEGNEMHEDVWVTKHNFQRTDVTYDIAVRLKTPITRNN 334

258 WVPICLPERFESERTLAFVRFSLVSGWQQLDRGATALEMVLNVPRLMQDCQLSRKV 317

335 VARACLPQKDWAEMLTQKIGIVSGFGRTHEKGROSNIKMLEVYPRNTC --- KL 389

318 GDSPIITEVMFCAGSGDSCKGSDGGPHATHRGTYWLTGIVSNGQCATVGHGCVY 377

390 STFSITONMFCAQEAKLEDACQGDGGPHVTRKNTYVVTGIVSWGEGCARKGKYGY 449

378 TRVSQVIELQKLMRSEPRP 397

450 TKVTFKLWIDRSNKAERVGP 469

RESULT 10

Q99L32 PRELIMINARY; PRT; 481 AA.

AC 099L32; DT 01-JUN-2001 (Tremblel. 17, Created)

DT 01-JUN-2002 (Tremblel. 17, Last sequence update)

DE Coagulation factor X.

F10

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10990;

RN [1]

RA SEQUENCE FROM N.A.

RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases

CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSI FAMILY.

DR EMBL; BC003877; AAH03877.1; -.

DR HSSP; P00742; 1XKA.

DR MEROPS; S01_216; -.

DR MGD; MGJ:103107; F10.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR01314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR00742; EGF_2.

DR InterPro; IPR01881; EGF_Ca..

DR InterPro; IPR01438; EGF_II.

DR InterPro; IPR00283; GLA_blood.

DR InterPro; IPR01254; Ser_protease_Try.

DR InterPro; IPR000794; VITK_dep_GLA..

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00534; gla; 1.

DR Pfam; PF00059; trypsin; 1.

DR PRINTS; PRO0072; CHYMTTRYPSIN.

DR PRINTS; PRO0010; EGBLOOD.

DR SMART; SM00011; GLABLOOD.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00001; EGF_like; 2.

DR SMART; SM0069; gla; 1.

DR SMART; SM00020; TRYSPC; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_Ca; 1.

RESULT 11

Q95ND6 PRELIMINARY; PRT; 461 AA.

AC 095ND6; DT 01-DEC-2001 (Tremblel. 19, Created)

DT 01-DEC-2001 (Tremblel. 19, Last sequence update)

DT 01-MAR-2002 (Tremblel. 20, Last annotation update)

DE Coagulation factor XI.

GN F9.

DR Pan troglodytes (Chimpanzee)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Homidae; Pan.

OX NCBI_TaxId=9598;

RN [1]

RA SEQUENCE FROM N.A.

RP STRAIN=505;

RA Satta Y.;

RT Comparison of DNA and protein polymorphisms between humans and chimpanzees";

RL Genes Genet. Syst. 0-0 (2001).

DR EMBL; AB062451; BAB5886.1; JOINED.

DR EMBL; AB062461; BAB5886.1; JOINED.

DR EMBL; AB062463; BAB5886.1; JOINED.

DR EMBL; AB062465; BAB5886.1; JOINED.

DR EMBL; AB062467; BAB5886.1; JOINED.

DR EMBL; AB062469; BAB5886.1; JOINED.

DR InterPro; IPR00052; Asx_hydroxyl.

DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR0181; EGF_Ca.
 DR InterPro; IPR01254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF000594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PROSITE; PS00022; EGF_HIDROXYL; UNKNOWN_1.
 DR PROSITE; PS01185; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_Ca; UNKNOWN_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE; PS05040; TRYPSIN_DOM; 1.
 DR PROSITE; PS0134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE: 461 AA; 51655 MW; 8F5A69A525DF65B5 CRC64;
 Query Match 37.7%; Score 825; DB 6; Length 461;
 Best Local Similarity 39.3%; Pred. No. 4.2e-72;
 Matches 163; Conservative 68; Mismatches 132; Indels 52; Gaps 9;
 OY 11 GLSLRCKXKXQCSFXKXARYKFKDAXRTKLFWISYSDGDOCASPCONGSCKKQDLS 70
 Db 58 GNLERCBMEEKCSFEEAREVFEVENTTETFWKQVGDQOCESNPLNGSCKKDINS 117
 OY 71 FCLPAFEGRNCETHKDDOLICVNINGGCQYCSDHTGKRSCHGEGYSLLAGVSCPT 130
 Db 118 WCPGEGEGRCKEL---DTCNCNKGRCBQFCKNSADNKVVCSTEGIRLAENQKSCPA 173
 OY 131 VEYVCGKIPPLEKRKNSK-----POG-----RIVGGKVC 159
 174 VPFPCGRVNSVQSOISKLTRAETVPPDVYVNSTAEITDNTTQTPQSSXXTHXVGEDX 233
 OY 160 PKGCPWQYLLVNGAQLCGGTINTIIVWSAHCDFK-IKNVRLNIALVGLGEIDLSEHDG 218
 Db 234 NPGQYPRKXVPLNGKWDAGCGGSIIVNEKVNITAAHCVDPGK---ITVAGHEHNTIEH 289
 219 DEQSRVAVQVITIYSTIVPGTT-NHDIALRLHQVPLVWPLHVVPLCPLERTSERTAFV 276
 OY 290 TECKKVNTRIIPPHNVMNAINKVNDIALLEDEPLVLYNSVYTPICADK--EYTNFL 346
 OY 277 RPL--SLVSGWQOLLDGTALEMVNLVPLPQDQKQSRKGDSNITEVMFCAGYSD 334
 Db 347 KFGSGYIVSGWGRYFHKGRSALVYQVLRYPLVDRATLSTKRF---TIVNNFCAGFHE 401
 OY 335 GSDSKCKDGGHATHYRGTMWLTGVWSWGCATCQHFGYTRYVTSQYIENLQK 389
 Db 402 GGRDSCQGDGGPHVTEVEGTSFLTGTSWGEBCAMKGKYGIVTKVSRVNMKE 456
 RESULT 12
 OYTTRO PRELIMINARY; PRT; 456 AA.
 ID OYTTRO
 AC OYTTRO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Protein C precursor.
 GN PROC.
 OS Canis familiaris (Dog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnerberg L.,
 RA Brenig B.;
 RT "Molecular characterization and chromosomal assignment of the canine
 RT protein C gene." Mamm. Genome 10:135-139(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99371952; PubMed=10443005;
 RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
 RT "Analysis of canine protein C gene polymorphisms";
 RL Anim. Genet. 30:237-238(1999).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL; AJ001979; CAM05126.1; .
 DR HSSP; P04070; 1PCU.
 DR MEROPS; S01.2.8; .
 DR InterPro; IPR000152; ASX_hydroxyl.
 DR InterPro; IPR0134; Chymotrypsin.
 DR InterPro; IPR00561; EGF-like.
 DR InterPro; IPR0181; EGF_Ca.
 DR InterPro; IPR0233; GLA_blood.
 DR InterPro; IPR01224; Ser_protease_Try.
 DR Pfam; PF00089; EGF; 2.
 DR Pfam; PF000594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO072; CHYMOTRYPSIN.
 DR PRINTS; PRO0001; GLABL0OD.
 DR SMART; SM0069; GLA; 1.
 DR SMART; SM0000; TRYSP; 1.
 DR SMART; SM0010; ASX_HIDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;
 KW Hydroxylation; Repeat; Serine protease; Signal; SIGNAL
 FT CHAIN 43 192 PROTEIN_C_LIGHT_CHAIN.
 FT CHAIN 193 194 PROTEIN_C_CONNECTING_DIPEPTIDE.
 FT CHAIN 195 455 PROTEIN_C_HEAVY_CHAIN.
 SQ SEQUENCE: 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;
 Query Match 36.4%; Score 796.5; DB 6; Length 456;
 Best Local Similarity 39.7%; Pred. No. 2.6e-69;
 Matches 165; Conservative 77; Mismatches 144; Indels 33; Gaps 11;

OY 1 ANAFLXXLRRPGSTXRXCKXXQCSFXKXARYKFKDAXRTKLFWISYSDGDOCAS----- 52
 Db 43 ANSFLETRRAGSLERECMEICDFEEKEIFONVDDTLAYNSKYVQDQCALPPHACD 102
 OY 53 SPCONGSCKKDQLOQSYICFCFLPAFEGRNCETHKDDOLICVNINGGCQYCSDHTGKRS 112
 Db 103 SPCCGHGSCIDGIGAHFCDCRGWEGRCQ-HEVSYINCSDLNGCSHYCLEEG-GRHC 160
 OY 113 RCHEGTISLADGQVSCPTVEPGK1-PILER-----NASPQGRIVGGKVC 162
 Db 161 SCAPGYRLQDDHLCQPAVKFCGRGKQMKKKRKLKRNOTDODIPRIVNGVTRG 220
 OY 163 ECPWQULLVNGAQ-GGTINTIIVWSAHCDFKTKKNRNLIAVLGEIDLSEHDG 221
 Db 221 ESPWQVLLDSSKKLACGAVIHTSVLTAHCMEDS--KLIRIGEIDLRREKGEM 277
 OY 222 SRRVAQVITIYSTVPGTNTIDIALRLHQVPLVLTQHVPCLPERFSENLTAFV-RFSI 280
 Db 278 DVIDKEVLIHPNSKSTTDNDIALLHLAQPAIFSOVTPICLPLDPSGLAERBLTQGOETV 337
 OY 281 VSGWQOLLD--RGATALELMLVNLVNRPLMTPCLOSRKVDKSPNTEYMCAGYSDGSK 338
 Db 338 VIGVGYRSETKRNRTEV-LPFTNIPVPHNECQIYNNM---1SENMCAGLGSRD 391
 OY 339 SCKGSGGPPATHYRGTMWLTGVWSWGCATVHFGVYVTRVQSQVIEWQKLMSE 394
 Db 392 ACEGDSGGPVFTSERGTMWLTGVWSWEGGGRHLHYGIVTKVSRVLDWHSIRGE 447

RESULT 13

Q28510 PRELIMINARY; PRT; 159 AA.

Q28510; PRELIMINARY; PRT; 159 AA.

AC 028510; PRELIMINARY; PRT; 159 AA.

DT 01-NOV-1996 (TREMBREL 01, Created)

DT 01-NOV-1996 (TREMBREL 01, Last sequence update)

DT 01-MAR-2002 (TREMBREL 20, Last annotation update)

DT Coagulation factor VII (Fragment).

DE Macaca mulatta (Rhesus macaque).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Macaca.

OC NCBI_TaxID=9544;

OC OK

RN RN

SEQUENCE FROM N.A.

[1]

RX MEDLINE=9422160; Pubmed=8168595;

RX Murakami M., Okamura T., Kuroiwa M., Harada M., Niho Y.; RT structures of the protease domains of mammalian blood coagulation factors VII and X. " Eur. J. Haematol. 52:162-168 (1994).

CC -I SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRPSIN FAMILY.

DR EMBL; D2121; BAA04753.1; -.

DR HSSP; P08709; IFRK.

DR MEROPS; S01_215; -.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001254; Serine_protease_Try.

DR Pfam; PF00089; TRYPSIN_1.

DR PRINTS; PRO0722; CHYMO TRYPSIN.

DR SMART; SM00020; TRYSPC; 1.

DR PROSITE; PS5040; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Hydrolease; Serine protease.

FT NON_TER 1

FT NON_TER 159 159

FT SQ SEQUENCE 159 AA: 17454 MW: 3F3EB82731B97DFC1 CRC64;

Query Match 35.2%; Score 769.5; DB 11; Length 460; Best Local Similarity 36.7%; Pred. No. 1.e-66; Matches 158; Conservative 79; Mismatches 152; Indels 41; Gaps 11; Mismatches 152; Indels 41; Gaps 11;

Qy 1 ANALXXRPGSXRXXKXXQCSXXAXXIFKDXAXRKLWISYSDQCAS----- 52

Db 42 ANSCLLEEMRPGSLERECMEICIDFEAEQEIQFWEDTLAFWIKYFDQDSCAPPDHOQ 101

Qy 53 SPCQNGGCKDQOLASQYICRCLPERFTRKDKDOLICVNGGEOQCSDTGKRC 112

Db 102 SPCQGHGTCIDGTSFSCDKWEGKFCQOELRFQCRVN-NGCILHYCLESENGRR-C 159

Qy 113 RCHEGYSLIADGVSCPTVEYPGKIP--ILEKRNASK-----POGRIVGKVC 160

Db 160 ACGRGYELADDHAKKCKSIVNPGKGLWIEKKRKLKDTELEPDRIVINGTLK 219

Qy 161 KGSCPWQYLIVLNGAQ-CGGTLLNTIVVSAHCFDKIKRNRLAVLGHEDLSHEDG 219

Db 220 QGSPWQWILDSKRRKLLQPVLTQVPLCPGLPERMFERTLW 276

Qy 220 EQRRVAVLPISTVWPTTNDIALLRQPVLTQVPLCPGLPERFTSERTLAVRS 279

Db 277 ELDIDIKBILVHPNVTSSRSDNDIALLRQAPATLSRTVPICPLNGLAELTQAOET 336

Qy 280 LIVSGWQOLD-----RGATALELMVNVPRMLTQDCLQSQSARVGDSPNITBYMCAGYS 333

Db 337 WTVWGGVQSDRIGRRRTI-LTFRIPVARNETEVWKNV---VSERNLCAII 390

Qy 334 DGSKDSCKDGGPHATHYRGTWLTLGIVSWSMOCATVGHGCVYTRYQSOWLQKLMRS 393

Db 391 GDTDACDGGPMVVFRGTVFLGLVSGEGCGHTNNYGIYTKVGSYLRKWHISYGE 450

Qy 394 EPRGVILRA 403

Db 451 K--GVSLKS 457

RESULT 14

Q91WN8 PRELIMINARY; PRT; 460 AA.

AC 091WN8; PRELIMINARY; PRT; 460 AA.

DT 01-DEC-2001 (TREMBREL 19, Created)

DT 01-DEC-2001 (TREMBREL 19, Last sequence update)

DE Similar to protein C.

GN PROC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RN [1]

RN Strauberg R.;

RL Submitted (SSP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013896; AAM13896.1; -.

DR MGDB; MGI_97771; PROC.

DR InterPro; IPR000152; Asp-Hydroxyl.

DR InterPro; IPR000561; EGF-Like.

DR InterPro; IPR001881; EGF-Ca.

DR InterPro; IPR00124; Serine_protease_Try.

DR Pfam; PF00088; EGF; 2.

DR Pfam; PF00594; gta; 1.

DR Pfam; PF00089; trypsin; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01187; EGF_CA; UNKNOWN_1.

DR PROSITE; PS00011; GLU_CARBONYLATION; UNKNOWN_1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.

KW Hydrolase; Serine protease.

SQ SEQUENCE 460 AA; 51818 MW; 017P26E68FCC274 CRC64;

Query Match 35.2%; Score 769.5; DB 11; Length 460; Best Local Similarity 36.7%; Pred. No. 1.e-66; Matches 158; Conservative 79; Mismatches 152; Indels 41; Gaps 11; Mismatches 152; Indels 41; Gaps 11;

Qy 1 ANALXXRPGSXRXXKXXQCSXXAXXIFKDXAXRKLWISYSDQCAS----- 52

Db 42 ANSCLLEEMRPGSLERECMEICIDFEAEQEIQFWEDTLAFWIKYFDQDSCAPPDHOQ 101

Qy 53 SPCQNGGCKDQOLASQYICRCLPERFTRKDKDOLICVNGGEOQCSDTGKRC 112

Db 102 SPCQGHGTCIDGTSFSCDKWEGKFCQOELRFQCRVN-NGCILHYCLESENGRR-C 159

Qy 113 RCHEGYSLIADGVSCPTVEYPGKIP--ILEKRNASK-----POGRIVGKVC 160

Db 160 ACGRGYELADDHAKKCKSIVNPGKGLWIEKKRKLKDTELEPDRIVINGTLK 219

Qy 161 KGSCPWQYLIVLNGAQ-CGGTLLNTIVVSAHCFDKIKRNRLAVLGHEDLSHEDG 219

Db 220 QGSPWQWILDSKRRKLLQPVLTQVPLCPGLPERMFERTLW 276

Qy 220 EQRRVAVLPISTVWPTTNDIALLRQPVLTQVPLCPGLPERFTSERTLAVRS 279

Db 277 ELDIDIKBILVHPNVTSSRSDNDIALLRQAPATLSRTVPICPLNGLAELTQAOET 336

Qy 280 LIVSGWQOLD-----RGATALELMVNVPRMLTQDCLQSQSARVGDSPNITBYMCAGYS 333

Db 337 WTVWGGVQSDRIGRRRTI-LTFRIPVARNETEVWKNV---VSERNLCAII 390

Qy 334 DGSKDSCKDGGPHATHYRGTWLTLGIVSWSMOCATVGHGCVYTRYQSOWLQKLMRS 393

Db 391 GDTDACDGGPMVVFRGTVFLGLVSGEGCGHTNNYGIYTKVGSYLRKWHISYGE 450

Qy 394 EPRGVILRA 403

Db 451 K--GVSLKS 457

RESULT 15

Q99PC6 PRELIMINARY; PRT; 460 AA.

AC 099PC6; PRELIMINARY; PRT; 460 AA.

DT 01-JUN-2001 (TREMBREL 17, Created)

DT 01-JUN-2001 (TREMBREL 17, Last sequence update)

DT 01-JUN-2002 (TREMBREL 21, Last annotation update)

DE Anticoagulant protein C.

GN PROC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE: FROM N.A.
 RC STRAIN=C7BL;
 RA Korf I.;

RT "Complete sequence of UC72A01."

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL; AF18182; AAK07918.1; -.

DR HSSP; P04070; Ipc0.

DR MEROPS; S01218; -.

DR MGI; MGI-9771; PROC.

DR InterPro; IPR000152; Asx-hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR00154; Ser_protease_TRY.

DR InterPro; IPR000294; VIT_K_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMO TRYPSIN.

DR PRINTS; PR0001; GLA_blood.

DR SMART; SM0001; EGF_Ca; 1.

DR SMART; SM0069; GLA; 1.

DR SMART; SM00020; TRY_P_SPC; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS00186; EGF_2; 2.

DR PROSITE; PS00187; EGF_Ca; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00024; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase;

KW Hydroxylation; Repeating Serine Protease;

SEQUENCE 460 AA; 5184 MW; 0293BC25E9D3ED16 CRC54;

Query Match

best Local_Similarity 36.5%; Pred. No. 4.4e-66;

Matches 157; Conservative 79; Mismatches 153; Indels 41; Gaps 11;

QY 1 ANAFLXXLRPGLRXXRCKAXYQCSXXARAKIFDKAXRTKLEFWISYSDGDOCAS----- 52

Db 42 ANSFLLEMRPGSLRERCBMCEBICLDEAOELFQMDTFLAFWIKYEDGQCSAPPDHQCD 101

QY 53 SPCQNGGSKDQSLQSYICLCLPATEGRNGETHKDQDLCVNERHGEQYQSDITGTKRSC 112

Db 102 SPCCGHGTCIDGIGSFSCCDKGNGEKGFCQQLERFQDCRVN-NQGCLHVCLEPESNGRR-C 159

QY 113 RCHCYSLLADGVSCTPTVYPCPKIP--I-LEKNAK-----POGRIVGGKVCP 160

Db 160 ACAPGYELADDHMRCKSTVNPCCGKLRGWRKIEKKRKLKRDIDLEDELPDPRTVNGTLK 219

QY 161 KGECPWQVQVLLVNGAQL-CGGTINTIIVWSAHCDFDKTKNWRNLIAVIGEHDSEHGD 219

Db 220 QGDSPWQATLDSKRLKLAGGVLHTSWLTAIC--VEGTRKLTVRLGEYDLRRDH 276

QY 220 EQSRRAQVITIPSTVPGITTNHDALLRHOVVLTDHVPLQPERFTSERTLAFVFRS 279

Db 277 ELDIDIKEILVHPIVYTRRSSNDNQDALLRLAQPATISKIVPICUPNNGLAQELTQAGET 336

QY 280 LVSGWQQLD----RGATALEMVLYNPRLMWDQCLQOSRQYGSNITEMFCAYS 333

Db 337 VVIGWGYQSDRICKDRGRRNRTFTI-LTFIRIPLVARNECVEMKIV-----VSENMCAGII 390

QY 334 DGSFDSCKDSDGGHATHYRGTMYLGLIVSWMGGCATVGHFGYTRVSOQIYEWLQKLRS 393

Db 391 GDTDADCGDGGPMVFFRGTVFLVGLWSBGGCHTNNGYITKVGSYSLKWHSYIGE 450

QY 394 EPRFCVLLRA 403

Db 451 R---GVSLKS 457

Search completed: July 1, 2003, 17:53:45
 Job time : 83 secs